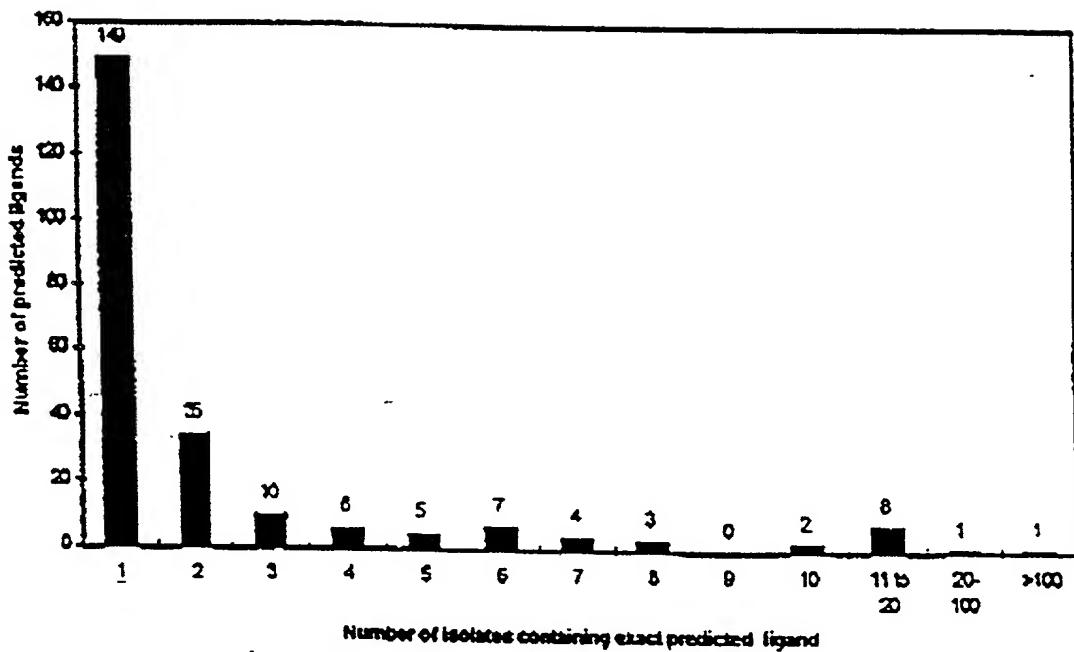


FIG. 1

a)



b)

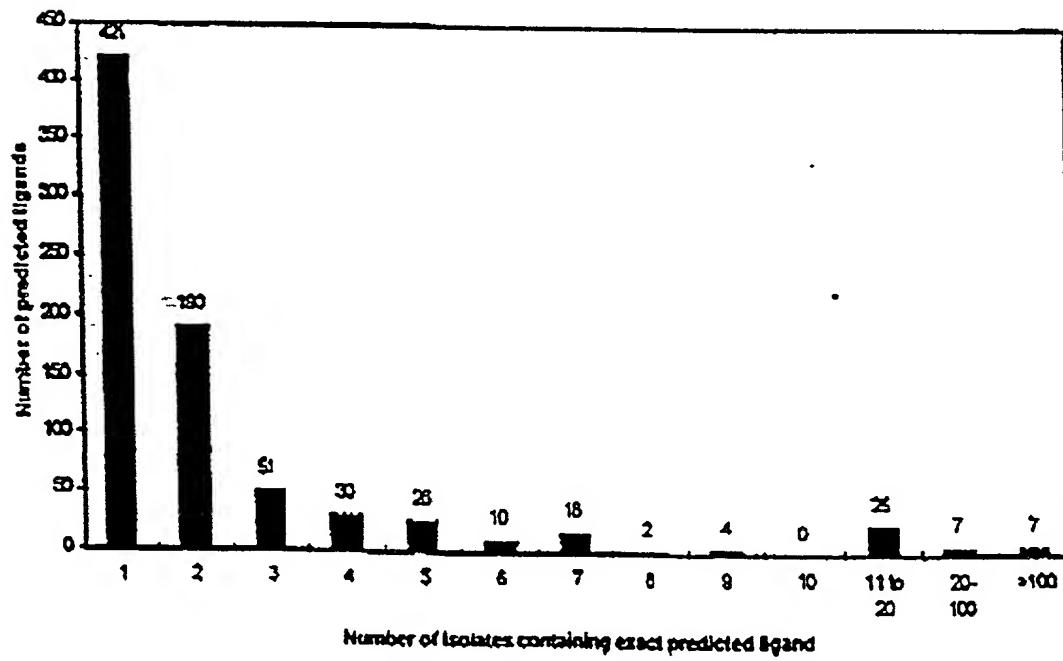
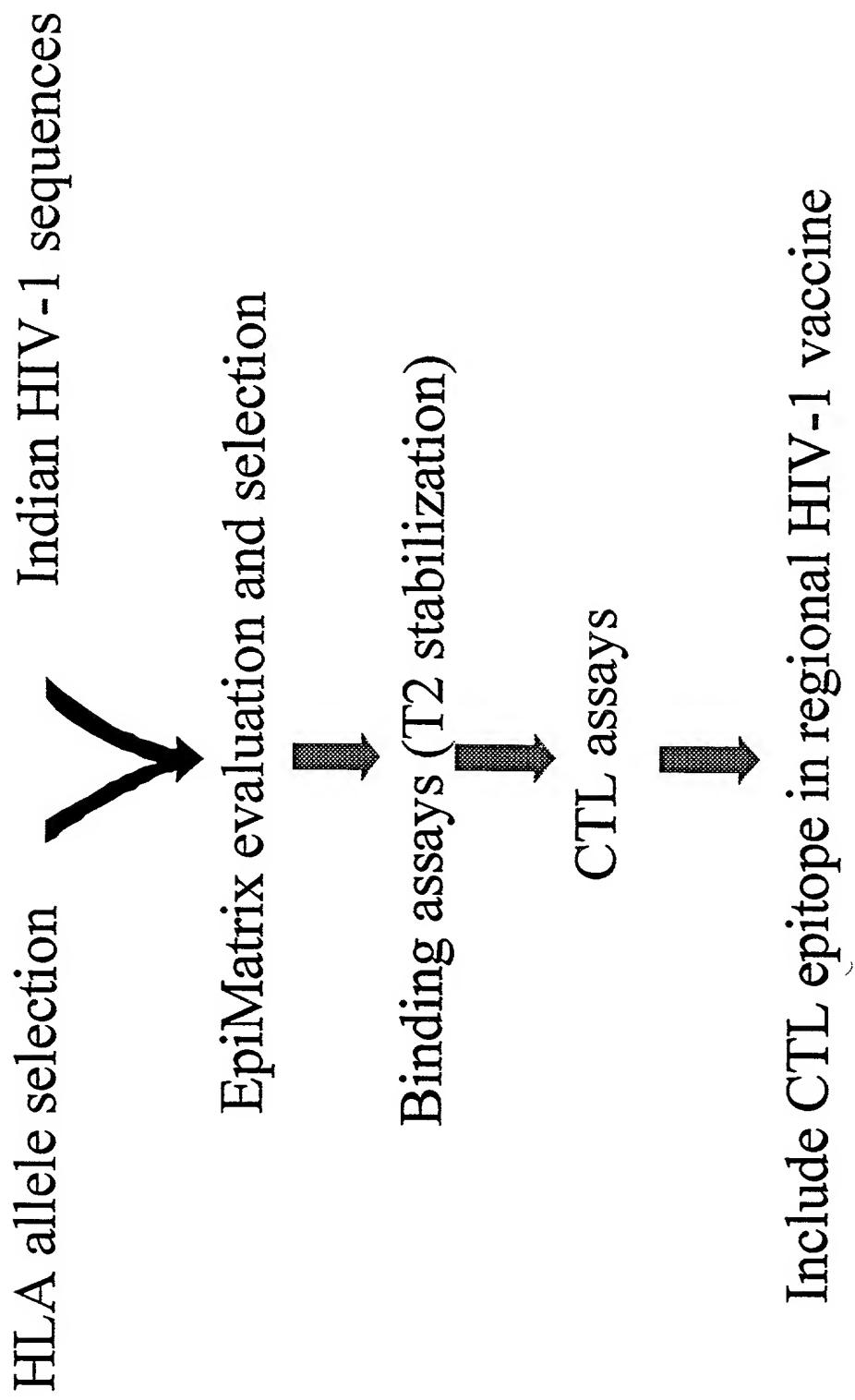


FIG. 2

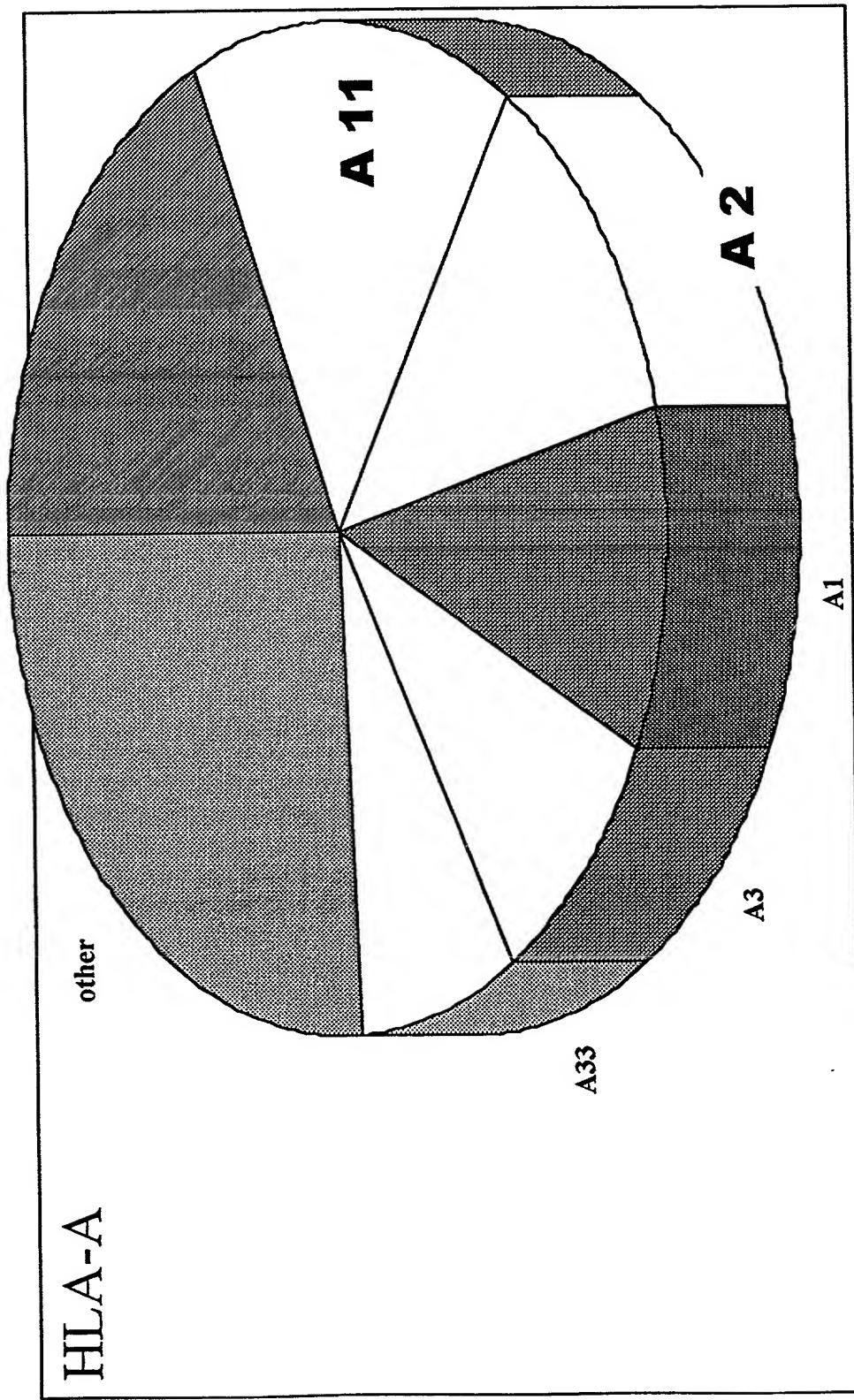
Sequence	A2 EBP	B27 EBP	A2 Fold Increase	B27 Fold Increase	Protein Isolates	Number of Approximate Position in	Clade A	Clade B	Clade C	Clade D	Clade E	Other SEQ ID NO.	
	(less than 1.3 not reported)	(less than 1.3 not reported)	with Exact AA	LAI	Sequence	159	gp120 - 120	X	X	X	X	X	1
KLTPLCVTLN	55.68%	0.00%	1.33		Env	36	gag - 215	X	X	X	X	X	2
AEWDRVRHPV	66.42%	0.00%	1.35		Gag	18	gag - 100	X	X	X	X	X	3
SLFNTVATL	62.00%	0.00%			Gag	17	RT - 354	X	X	X	X	X	4
ELHPDKWTV	57.03%	0.00%			RT	17							5
GMDPPEREVL	72.52%	0.00%			Nef	17	nef - 170	X	X	X	X	X	6
GMDPPEKEVL	87.51%	0.01%	2.7		Nef	16	nef - 170	X	X	X	X	X	7
HLWRWGTMLL	76.69%	0.00%	1.33		Env	10	gp120 - 30	X	X	X	X	X	8
LLLTTRDGGVN	55.68%	0.00%			Env	>10	gp120 - 452	X	X	X	X	X	9
HLWKWSTMLL	90.92%	0.00%	1.63		Env	>10	gp120 - 20	X	X	X	X	X	10
ILKEPVHGV	97.47%	0.00%	1.54		RT	>10	RT - 480	X	X	X	X	X	11
KRWLGLNK	0.00%	14.22%	3.61		Gag	79	gag - 263	X	X	X	X	X	12
CRIKQIN	0.00%	99.08%			Env	185	gp120 - 420	X	X	X	X	X	13
CRIKQINMW	0.00%	99.52%	1.74		Env	150	gp120 - 420	X	X	X	X	X	14
VSFEPPIHF	0.20%	55.61%	1.45		Env	109	gp120 - 215	X	X	X	X	X	15
RCSSNNTGL	0.01%	62.11%			Env	101	gp120 - 446	X	X	X	X	X	16
VSFEPPIHY	0.00%	98.22%			Env	101	gp120 - 215	X	X	X	X	X	17
CRIKQINNM	0.00%	91.33%			Env	75	gp120 - 420	X	X	X	X	X	18
IRSENNTNN	0.00%	82.77%			Env	42	gp120 - 275	X	X	X	X	X	19
IRFIMV	0.05%	89.06%			Env	19	gp41 - 175	X	X	X	X	X	20
ISFDPIPHY	0.01%	67.49%			Env	15	gp120 - 215	X	X	X	X	X	21
YRTGDIIG	0.00%	56.14%			Env	15	gp120 - 330	X	X	X	X	X	22
IRIGPGQTFY	0.07%	75.36%			Env	13		X	X	X	X	X	23
GCGCKIC	0.00%	61.09%			Env	12	gp41 - 90	X	X	X	X	X	24
RRRAPQDS	0.00%	67.49%			Tat	12		X	X	X	X	X	25
IRSENNTDN	0.00%	59.28%			Env	11	gp120 - 275	X	X	X	X	X	26
CRKQFIN	0.00%	76.92%	1.53		Env	<10	gp120 - 420	X	X	X	X	X	27
KRISIGPGR	0.00%	56.93%	1.78		Env	<10	gp120 - 320	X	X	X	X	X	28
GCQQQIEQL	0.10%	78.95%			Env	<10	gp41 - 270	X	X	X	X	X	29
GRRGWELKY	0.01%	59.80%	3.27		Env	<10							

FIG. 3

Project Outline

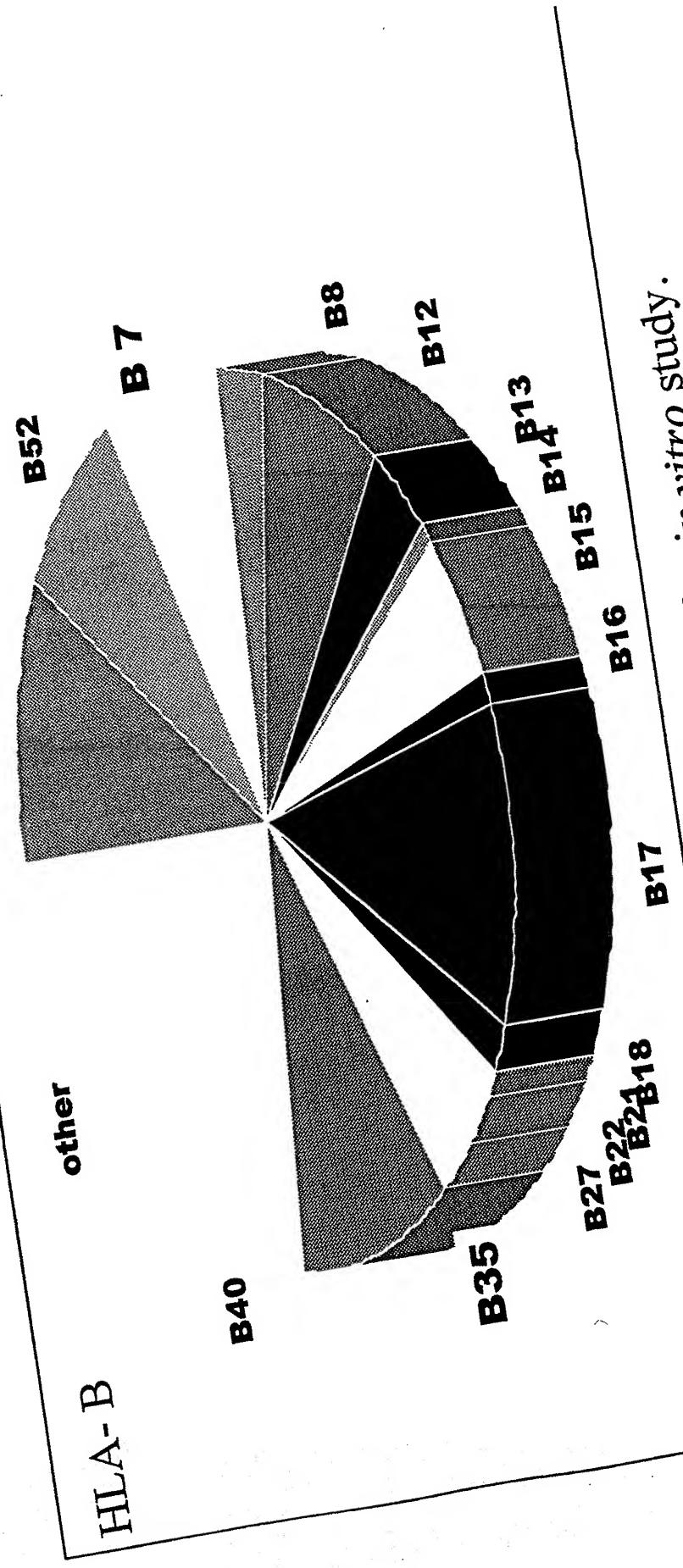


Methods: HLA allele selection



HLA-A2 and -A11, -B7 and -B35 were selected for this pilot project due their prevalence of the HLA alleles in the Indian population....

Methods: HLA allele selection



... and availability of cell lines for *in vitro* study.

FIG. 6
EpiMatrix Predictions and Binding Results: B 7
6 out of 7, and control peptide

B7							predicted EBF			avg MFI (200ug/ml)			avg fold incr. (20ug/ml)		
Peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL								
1	RPNNNNTRKSI	RPNNNNTRKSI	ENV	DID757	183-192	75	Y	8%	20%	335.6			2.4		
3	NPYNTPIFAL	NPYNTPIFAL	POL	SolInd5	61-70	60			20%	281.9			2.0		
4	RAIEAQQHLL	RAIEAQQHLL	ENV	Did747	481-490	60			17%	181.5			1.3		
5	TCKSNITGLL	TCKSNITGLL	ENV	Did760	375-384	59			18%	160.5			1.2		
	KPVVSTQLL	KPVVSTQLL	ENV	Did747	182-191	71			46%	248.5			1.8		
	KPCVKLTPL	KPCVKLTPL	ENV	Did747	51-60	100			27%	373.8			2.7		
	GPKVKQWPLT	GPKVKQWPLT	POL	SolInd4	25-34	100			27%	314.7			2.3		
	YPGIKVRLQL	YPGIKVRLQL	POL	SolInd4	278-287	100			26%	378.4			2.7		

FIG. 7
EpiMatrix Predictions and Binding Results: B 35
7 out of 7 ... and control peptide

B37		peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted CTL	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
peptide #	seq. Used	start-stop	% conserved	CTL	predicted CTL							
2	TVLDVGDAYF	TVLDVGDAYF	POL	Solnd4	114-123	100	Y	4%	47.9			1.6
6	EPPFLWMGY	EPPFLWMGY	POL	Solnd4	231-239	100		9%	48.7			1.6
7	VPVKLKGGM	VPVKLKGGM	POL	Solnd4	15-24	100		9%	53.3			1.7
8	CPKVTFDPI	CPKVTFDPI	ENV	DID760	144-153	53		7%	35.0			1.2
	KPVVSTQLL	KPVVSTQLL	ENV	DID747	182-191	71		9%	40.5			1.4
	KPCVKLTPLC	KPCVKLTPLC	ENV	DID747	51-60	100		11%	52.1			1.7
	GPKVKQWPLT	GPKVKQWPLT	POL	Solnd4	25-34	100		11%	41.2			1.4
	YPGIKVRLQL	YPGIKVRLQL	POL	Solnd4	278-287	100		7%	40.7			1.3

FIG. 8
EpiMatrix Predictions and Binding Results: A 2
3 out of 7 ... and control peptide

A2		peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBFI	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
13			ILKEPVHGV	ILKEPVHGVY	POL	SolInd4	316-325	80	Y	96%	1604.2	1.6
14			QLPEKDSWTV	QLPEKDSWTV	POL	SolInd4	252-261	100		87%	1368.1	1.4
15			NLWTVYYGV	NLWTVYYGV	ENV	GrD1024	32-41	67		84%	1716.9	1.8
16			QMHEDVISL	QMHEDVISLW	ENV	DiD747	37-46	91		78%	1413.1	1.4
17			KIEELREHLL	KIEELREHLL	POL	SolInd5	208-217	60		79%	889.9	0.9
18			DMVNQNMHEDV	DMVNQNMHEDV	ENV	DiD747	33-42	64		77%	731.1	0.4
19			GLKKKKSVTV	GLKKKKSVTV	POL	SolInd4	106-115	100		76%	1088.4	1.1
20			ELHPDKWTVQ	ELHPDKWTVQ	POL	SolInd4	240-249	80		72%	1048.1	1.0

FIG. 9
EpiMatrix Predictions and Binding Results: A 11
4 out of 7 ... and control peptide

A11								avg MFI (200ug/ml)		avg fold incr. (20ug/ml)	
Peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	Predicted EBF	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)	
21	IYQEPFKNLK	IYQEPFKNLK	POL	SolInd4	348-357	100	Y	7%	677.5	3.1	
22	VTFDPIPHY	VTFDPIPHY	ENV	DiD760	147-156	53		22%	190.0	0.9	
23	TVQCTHGIK	TVQCTHGIK	ENV	DiD747	174-183	59		44%	733.4	3.3	
24	NTPIFALKKK	NTPIFALKKK	POL	SolInd5	64-73	60		44%	187.8	0.9	
25	LVDFRELNK	LVDFRELNK	POL	SolInd4	81-90	100		47%	755.2	3.4	
26	PGMDGPVKV	PGMDGPVKV	POL	SolInd4	21-30	100		52%	193.8	0.7	
27	GIPHPAGLKK	GIPHPAGLKK	POL	SolInd4	100-109	100		62%	309.6	1.4	
28	FTTPDKKKHQK	FTTPDKKKHQK	POL	SolInd4	221-330	100		63%	920.6	4.1	

FIG. 10

Methods: T2 Binding Assay

Allele matched peptides stabilize MHC molecules on the surface of TAP deficient cells. The stabilized MHC-peptide complex is detected using Ab to the MHC and fluorescence labeled secondary Ab.

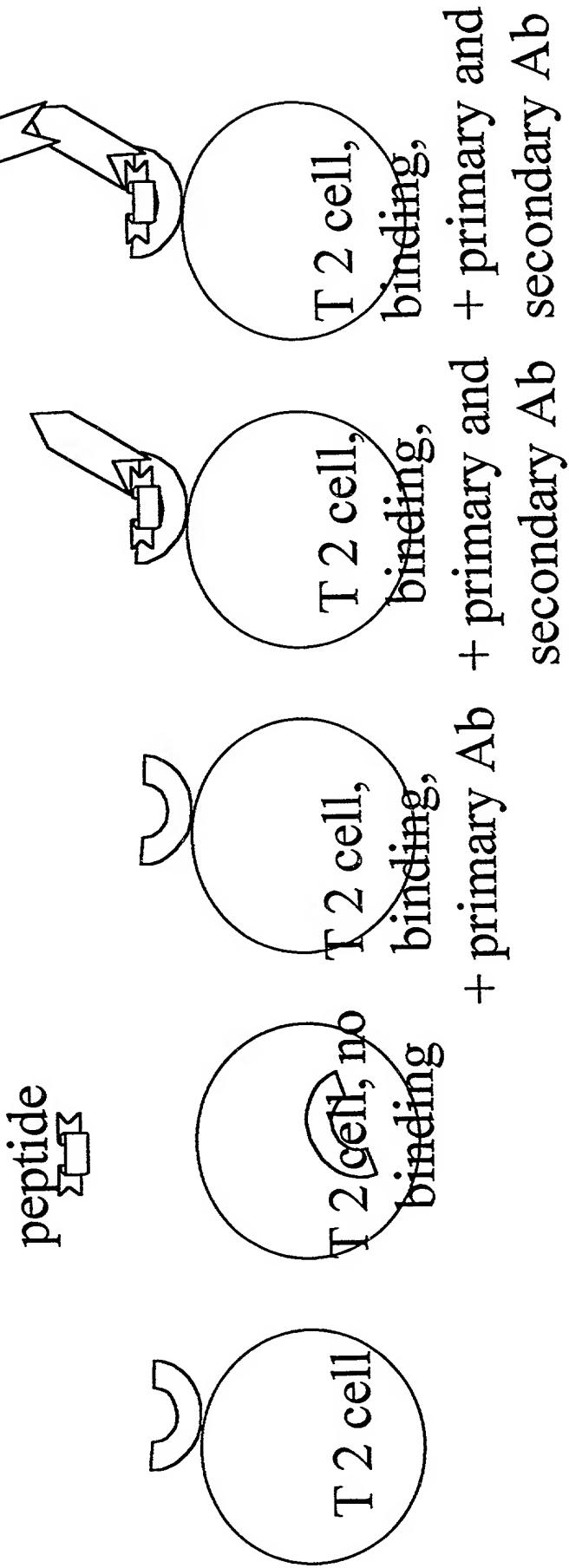


FIG. 11
Clustering of putative MHC ligands in *env*

